

1 / 10

COPY OF PAPERS
ORIGINALLY FILED

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTTCGATACCGAAACCACCGGTATGAACCAGATTGGT 75
M T A M S T A I T R Q I V L D T E T T G M N Q I G
GCGCACTATGAAGGCCACAAAGATCATTGAGATTGGTGCCGTTGAAGTGGTGAACCGTCGCCCTGACGGGCAATAAC 150
A H Y E G H K I I E I G A V E V V N R R L T G N N
TTCATGTTTATCTCAAAACCGATCGGCTGGTGATCCGGAAGCCCTTGGCGTACATGGTATTGCCGATGAATTT 225
F H V Y L K P D R L V D P E A F G V H G I A D E F
TTGCTCGATAAGCCACGTTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTCGCGGCGGAGTTGGTGATC 300
L L D K P T F A E V A D E F M D Y I R G A E L V I
CATAACGACGCTTCGATATCGGCTTATGGACTACGAGTTTCGTGCTTAAGCGCGGATATCCGAAGACCAAT 375
H N A A F D I G F M D Y E F S L L K R D I P K T N

FIG.-1A

2 / 10

ACTTTCGTAAAGGTCACCGATAGCCCTTGGGTGGCAGGAGAAATGTTTCCCGTAAGCGCAACAGCCTCGATGCG 450

mutD

T F C K V T D S L A V A R K M F P G K R N S L D A

TTATGIGCTCGCTACGAAATAGATAACAGTAAACGAACGCTGCACGGGGCATTACTCGATGCCAGATCCTTGCG 525

mutD

L C A R Y E I D N S K R T L H G A L L D A Q I L A

GAAGTTTATCTGGCGATGACCGGTGGTCAACGTCGATGGCTTTTGGCATGGAAGGAGAGACACACAGCAACAA 600

mutD

E V Y L A M T G G Q T S M A F A M E G E T Q Q Q Q

GGTGAAGCAACAATTTCAGCGCATTGTACGTCAGGCAAGTAAGTTACGCGTGTGTTTTGCGACAGATGAAGAGATT 675

mutD

G E A T I Q R I V R Q A S K L R V V F A T D E E I

GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAAGCGGGAAGTTGCCTCTGGCGAGCATAA 741

mutD

A A H E A R L D L V Q K K G G S C L W R A .

FIG. 1B

3 / 10

10	ATGAGCTATCGTATGTTTGAATTAATCTGGTTCCAAATGTTGAACCTTCTTTTGGCCCGGGCGCC	Eb_429T.dna
10	ATGAGCTATCGTATGTTTGAATTAATCTGGTTCCAAATGTTGAACCTTCTTTTGGCCCGGGCGCC	Eb_GEBT.dna
70	GTTTCTGTTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAAAAGCCCTGCTGGTGACC	Eb_429T.dna
70	GTTTCTGTTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAAAAGCCCTGCTGGTGACC	Eb_GEBT.dna
130	GATAAGGGCCCTGCGCGGCCATTAAAGACGGTGCTGTCGATCAGACCGTGAAAGCACCTGAAA	Eb_429T.dna
130	GATAAGGGCCCTGCGCGGCCATTAAAGACGGTGCTGTCGATCAGACCGTGAAAGCACCTGAAA	Eb_GEBT.dna
190	GCGCGCCGGTATTGAGGGTGGTCAATTTTCGACGGGGTCCGAGCCGAAACCCGAAAGACACCAAC	Eb_429T.dna
190	GCGCGCCGGTATTGAGGGTGGTCAATTTTCGACGGGGTCCGAGCCGAAACCCGAAAGACACCAAC	Eb_GEBT.dna
250	GTGCTCGACGGCCCTGGGCCATGTTCCCGTAAGAGCAGTGCGGACATGATAATCACCGTCGGC	Eb_429T.dna
250	GTGCTCGACGGCCCTGGGCCATGTTCCCGTAAGAGCAGTGCGGACATGATAATCACCGTCGGC	Eb_GEBT.dna

FIG.--2A

4 / 10

310	GGCGGCAGCCCGGCA	320	330	340	350	360	
310	GGCGGCAGCCCGGCTCGACTGCGGTAAGGCATTGGGTA						Eb_429T.dna
310	GGCGGCAGCCCGGCTCGACTGCGGTAAGGCATTGGGTA						Eb_GEBT.dna
370	CTGTACAGCTATGCCCGGTATCGAAACACTCACCAACCCGCTGCCGCGCCCATTA	380	390	400	410	420	
370	CTGTACAGCTATGCCCGGTATCGAAACACTCACCAACCCGCTGCCGCGCCCATTA						Eb_429T.dna
370	CTGTACAGCTATGCCCGGTATCGAAACACTCACCAACCCGCTGCCGCGCCCATTA						Eb_GEBT.dna
430	AACACCAACCGCCGGGACCGCCAGCGGAAGTCAACCCGCGCACTGCGGTGCTGACTAACACCAAA	440	450	460	470	480	
430	AACACCAACCGCCGGGACCGCCAGCGGAAGTCAACCCGCGCACTGCGGTGCTGACTAACACCAAA						Eb_429T.dna
430	AACACCAACCGCCGGGACCGCCAGCGGAAGTCAACCCGCGCACTGCGGTGCTGACTAACACCAAA						Eb_GEBT.dna
490	ACCAAAGTAAATTTGTGATTGTCAAGCTGGCGGCAACCTGCCCTTCCGCTCTCCATTAAACGAT	500	510	520	530	540	
490	ACCAAAGTAAATTTGTGATTGTCAAGCTGGCGGCAACCTGCCCTTCCGCTCTCCATTAAACGAT						Eb_429T.dna
490	ACCAAAGTAAATTTGTGATTGTCAAGCTGGCGGCAACCTGCCCTTCCGCTCTCCATTAAACGAT						Eb_GEBT.dna
550	CCGCTGCTGATGATCGGGCAAGCCCGCGCGGCTGACCGCGCGCGGTA	560	570	580	590	600	
550	CCGCTGCTGATGATCGGGCAAGCCCGCGCGGCTGACCGCGCGCGGTA						Eb_429T.dna
550	CCGCTGCTGATGATCGGGCAAGCCCGCGCGGCTGACCGCGCGCGGTA						Eb_GEBT.dna

FIG._2B

5/10

	610	620	630	640	650	660	
610	ACCCACGCGGTAGAGGCGCTATATCTCCAAAGACGCCAAACCCCGGTTACCGATGCTCTGCT						Eb_429T.dna
610	ACCCACGCGGTAGAGGCGCTATATCTCCAAAGACGCCAAACCCCGGTTACCGATGCTCTGCT						Eb_GEBT.dna
	670	680	690	700	710	720	
670	ATTACGGCCATCAAACTGATTGCGCCACCAACTTGGCGCCAGGCCCGTCCGCCCTGGGGACCAAC						Eb_429T.dna
670	ATTACGGCCATCAAACTGATTGCGCCACCAACTTGGCGCCAGGCCCGTCCGCCCTGGGGACCAAC						Eb_GEBT.dna
	730	740	750	760	770	780	
730	CTCAAAGCCCGTGAAACAATGGCCCTGGCCCTCTCTGCTGGCCGGGATGGCCCTTTAAACAAC						Eb_429T.dna
730	CTCAAAGCCCGTGAAACAATGGCCCTGGCCCTCTCTGCTGGCCGGGATGGCCCTTTAAACAAC						Eb_GEBT.dna
	790	800	810	820	830	840	
790	GCCAACCTGGGCTATGTTCACGCCCATGGCTCACCAAGCTGGCGCGGCTGTACGACATGGCC						Eb_429T.dna
790	GCCAACCTGGGCTATGTTCACGCCCATGGCTCACCAAGCTGGCGCGGCTGTACGACATGGCC						Eb_GEBT.dna
	850	860	870	880	890	900	
850	CACGGGGTGGCGGAACGCGGCTCCTGCTGCCGCCCATGTCTGCCGCTATAACCTGATTGCCAAC						Eb_429T.dna
850	CACGGGGTGGCGGAACGCGGCTCCTGCTGCCGCCCATGTCTGCCGCTATAACCTGATTGCCAAC						Eb_GEBT.dna

FIG._2C

6/10

910	920	930	940	950	960	
910	CCGGAAAAATTTGCCGATATCGCCACCTTTATGGGGGAAACAACACCCGGTCTTCCACC					Eb_429T.dna
910	CCGGAAAAATTTGCCGATATCGCCACCTTTATGGGGGAAACAACACCCGGTCTTCCACC					Eb_GEBT.dna
970	980	990	1000	1010	1020	
970	ATGGACGCAGCGGAGCTGGCCATCAGCGCCCATTTGCCCGTCTGTCTAAAGATGTCGGGATC					Eb_429T.dna
970	ATGGACGCAGCGGAGCTGGCCATCAGCGCCCATTTGCCCGTCTGTCTAAAGATGTCGGGATC					Eb_GEBT.dna
1030	1040	1050	1060	1070	1080	
1030	CCGCAGCACCTGCGTGAACTGGGGGTAAAGAGGCGGACCTTCCCGTACATGGCAGAAATG					Eb_429T.dna
1030	CCGCAGCACCTGCGTGAACTGGGGGTAAAGAGGCGGACCTTCCCGTACATGGCAGAAATG					Eb_GEBT.dna
1090	1100	1110	1120	1130	1140	
1090	GCCCTGAAGACGGCAACGCCCTTCTCTAACC CGCGCAAGGGAAACGAAATGCTTCCC					Eb_429T.dna
1090	GCCCTGAAGACGGCAACGCCCTTCTCTAACC CGCGCAAGGGAAACGAAATGCTTCCC					Eb_GEBT.dna
1150	1160	1170				
1150	GACATTTTCCGCCAGGCATTCTGA					Eb_429T.dna
1150	GACATTTTCCGCCAGGCATTCTGA					Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG._2D

7 / 10

	10	40	70	100	
10	MSYRMFDYLV	PNVNFF	GP	AVSVVG	QRCQLLGKKALLVT Eb_429T.dna
10	MSYRMFDYLV	PNVNFF	GP	AVSVVG	QRCQLLGKKALLVT Eb_GEBT.dna
	130	160	190	220	
130	DKGLRAIK	DGAVDQ	TVKHLKA	AGIEVVIF	DGV
130	DKGLRAIK	DGAVDQ	TVKHLKA	AGIEVVIF	DGV
	250	280	310	340	
250	VLDGLAM	FRKEQC	DMIITV	GGGSPH	DCGKGIGIAATHPGD Eb_429T.dna
250	VLDGLAM	FRKEQC	DMIITV	GGGSP	LDCGKGIGIAATHPGD Eb_GEBT.dna
	370	400	430	460	
370	LYSYAGIE	TLTNPL	PPPIIA	VNTTAGT	ASEVTRHCVLTNTK Eb_429T.dna
370	LYSYAGIE	TLTNPL	PPPIIA	VNTTAGT	ASEVTRHCVLTNTK Eb_GEBT.dna
	490	520	550	580	
490	TKVKFVI	SVWRNLP	SVSIND	P	LLMIGKPA
490	TKVKFVI	SVWRNLP	SVSIND	P	LLMIGKPA

FIG._3A

8 / 10

	610	640	670	700	
610	THAVEAYISKDANPVTDASAIQAIKLIATNLRQAVALGTN				Eb_429T.dna
610	THAVEAYISKDANPVTDASAIQAIKLIATNLRQAVALGTN				Eb_GEBT.dna
	730	760	790	820	
730	LKARENMACASLLAGMAFNANLGYVHAMAHQLGGLYDMA				Eb_429T.dna
730	LKARENMACASLLAGMAFNANLGYVHAMAHQLGGLYDMA				Eb_GEBT.dna
	850	880	910	940	
850	HGVANAVLLPHVCRYNLIANPEKPFADIAITFMGENTTGLST				Eb_429T.dna
850	HGVANAVLLPHVCRYNLIANPEKPFADIAITFMGENTTGLST				Eb_GEBT.dna
	970	1000	1030	1060	
970	MDAAELAISAIARLSKDVGI PQHLRELGVKEADFFPYMAEM				Eb_429T.dna
970	MDAAELAISAIARLSKDVGI PQHLRELGVKEADFFPYMAEM				Eb_GEBT.dna
	1090	1120	1150		
1090	ALKDGNAPSNPRKGNKEKEIADIFRQAF				Eb_429T.dna
1090	ALKDGNAPSNPRKGNKEKEIADIFRQAF				Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG._3B

9 / 10

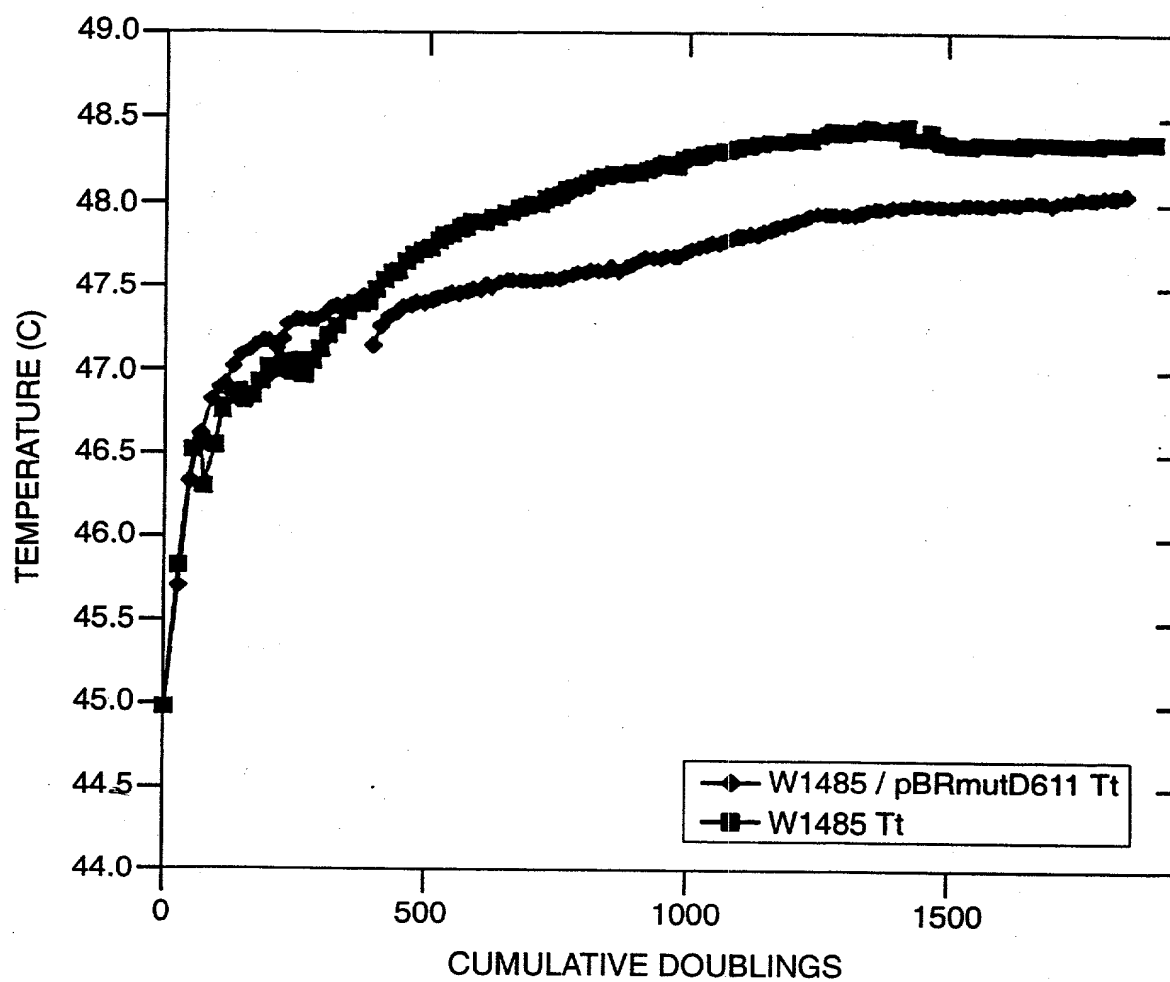


FIG._4

10 / 10

